<Bioinformatics Center> Bioknowledge Systems

Bioinformatics Center
- Bioknowledge Systems -

http://kanehisa.kuicr.kyoto-u.ac.jp/

Prof
KANEHISA, Minoru
(D Sc)

Assoc Prof
GOTO, Susumu
(D Eng)

Assist Prof
HATTORI, Masahiro
(D Sc)

Assist Prof (AIGC)
ITOH, Masumi
(D Sc)

Assist Prof (COE)
YAMANISHI, Yoshihiro
(D Sc)

Assist Prof (AIGC)
TOKIMATSU, Toshiaki
(D Agr)

PD
HAYES, Nelson
(Ph D)

PD
GUTTERIDGE, Alexander
(Ph D)

PD
RUIZ, Diego Deiz
(Ph D)

PD
OKUDA, Shujiro
(D Sc)

PD
LIMVIPHUVADH, Vachiranee
(D Sc)

PD
FUJITA, Masashi
(D Sc)

Research Associate (pt)

MORIYA, Yuki

Researcher

HIRAKAWA, Mika

Students

SAKIYAMA, Tadahiko (D3)
ONUKI, Ritsuko (D3)
SHIGEMIZU, Daichi (D3)
HONDA, Wataru (D2)
HASHIMOTO, Kosuke (D2)
MUTO, Ai (D2)
SUGA, Akitsugu (D2)
TANAKA, Michihiro (D1)
TAKARABE, Masataka (D1)
SHIMIZU, Yugo (M2)
MIZUTANI, Sayaka (M1)
HIRANUKA, Kazushi (M1)
KOBAYASHI, Takeshi (M1)

Scope of Research

DNA, RNA, and proteins are the basic molecular building blocks of life, but the living cell contains additional molecules, including water, ions, small chemical compounds, glycans, lipids, and other biochemical molecules, without which the cell would not function. Because the proteins responsible for biosynthesis, biodegradation, and transport of these additional molecules are encoded in the genome, one may assert that all cellular functions are specified by the genomic DNA sequence. In practice, however, it is not possible to infer higher-level systemic functions of the cell or the organism simply from the molecular sequence infomation alone. We are developing bioinformatics methods to integrate different types of data and knowledge on various aspects of the biological systems towards basic understanding of life as a molecular interaction/reaction system and also for practical applications in medical and pharmaceutical sciences.

Research Activities (Year 2007)

Grants

Kanehisa M, Education and Research Organization for Genome Information Science, MEXT.

Kanehisa M, Knowledge Information Infrastructure for Genome Information Science, Kyoto University 21st Century COE Program, MEXT.

KEGG RPAIR Database and Prediction of Biodegradation Pathways

In this study, we focus on the biodegradation pathways of xenobiotics in bacteria. First, we perform a systematic survey of the KEGG RPAIR database containing chemical structure alignments of substrate-product pairs and chemical structure transformation patterns in all known enzyme-catalyzed reactions. Biochemical structure transformations are described by what we call RDM patterns, which represent KEGG atom type changes at the reaction center atom (R) and its neighbouring atoms on the different region (D) and the matched region (M). Second, we present a method to predict potential biodegradation pathways of xenobiotics. The RDM patterns presumably represent the reaction specificity of enzymes, but not the substrate specificity. Therefore, in our prediction system a new compound is first compared against all known substrate and product structures, and then possible RDM patterns are selected by considering the similarity scores of matched compounds. By limiting the dataset to bacterial reactions appearing in the "Xenobiotics Biodegradation and Metabolism" category of the KEGG PATHWAY database, this prediction system can be adjusted to microbial biodegradations.

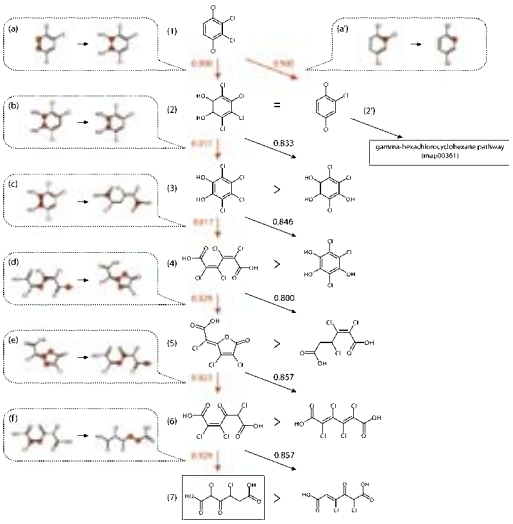

Figure 1. The prediction of 1,2,3,4-tetrachlorobenzene biodegradation pathway. The query compound (1) is transformed to compounds (2)–(7) with the transformation patterns of matching compounds (a)–(f). The reactions in the dotted boxes show the transformation patterns of the best matching compounds (a)-(f), where the reaction center atoms are marked with red circles.

The Commonality of Protein Interaction Networks Determined in NDDs

Neurodegenerative disorders (NDDs) are progressive and fatal disorders, which are commonly characterized by the intracellular or extracellular presence of abnormal protein aggregates. Here, we first investigated the commonality among the six NDDs from the molecular point of view. By reviewing published literatures in PubMed, we created pathway maps in KEGG for binary relations in six NDDs: Alzheimer's disease (AD), Parkinson's disease (PD), amyotrophic lateral sclerosis (ALS), Huntington's disease (HD), dentatorubral-pallidoluysian atrophy (DRPLA) and prion disease (PRION). We also collected data on 201 interacting proteins and 13 compounds with 282 interactions from the literature. We found 19 proteins common to these six NDDs. These common proteins were mainly involved in the apoptosis and MAPK signaling pathways. We also expanded the interaction network by adding protein interaction data from the Human Protein Reference Database and gene expression data from the Human Gene Expression Index Database and finally we found 174 common proteins and 202 common interactions. We then carried out domain analysis on the extended network and found the characteristic domains, such as 14-3-3 protein, phosphotyrosine interaction domain and caspase domain, for the common proteins. Moreover, PD and HD showed the highest correlation in terms of domain distributions and we found the commonality in the tight junction pathway, which has not previously been associated with the mechanism of either disease.

Figure 2. 174 common proteins and 202 common interactions found in the extended network of NDDs.

Kanehisa M, Backbone Database for Analysis of the Biological Systems and Environment, Grant-in-Aid for Scientific Research on Priority Areas, MEXT.

Kanehisa M, Deciphering Systemic Biological Functions by Integration of Genomic and Environmental Information, Bioinformatics Research and Development, JST.

Kanehisa M, Hierarchical Structuring and Integration of Knowledge in Life Sciences, Integrated Database Project, MEXT.

Kanehisa M, Integration of Genomics and Chemistry in Glycome Informatics, NIH, USA.